

Does Telomere Length Explain Race/Ethnic Differences in Aging among Older Adults?: Evidence from the Health and Retirement Study



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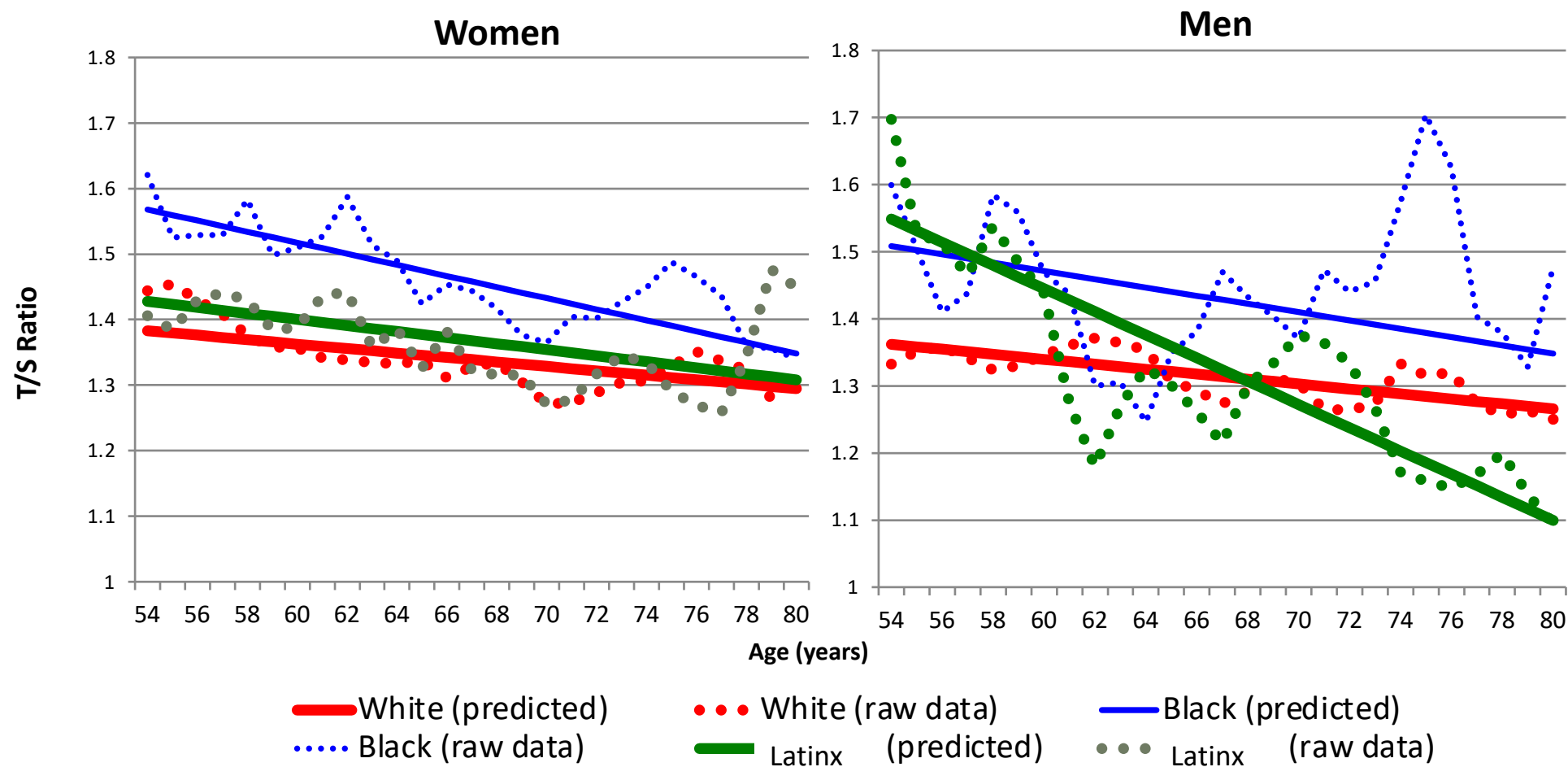
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Health & Retirement Study: Older Blacks & Latinx adults have longer Salivary TL (STL) than whites (n=5,228) (Brown, Needham & Ailshire, 2017)



Gender differences in TL

- Women have long TL than men (see Gardner et al, 2014 for a review)

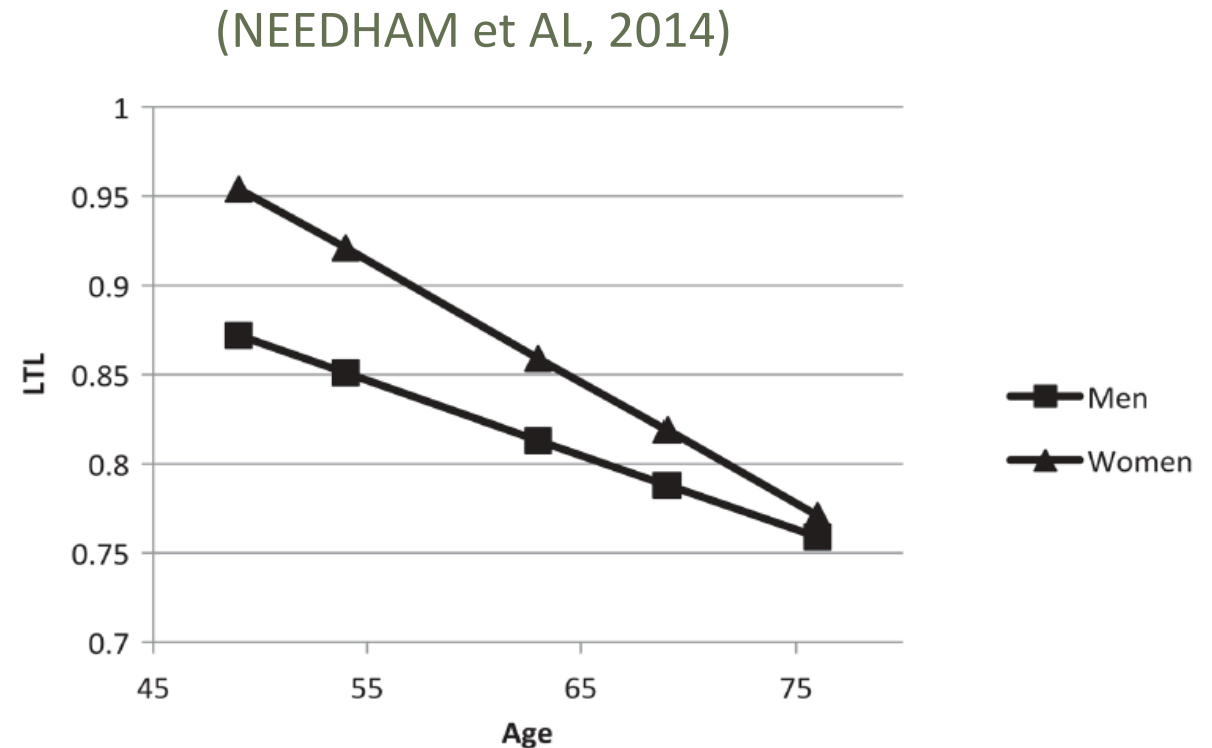


Figure 2.
LTL (T/S ratio) by gender and age ($n = 851$).

Mixed Findings: TL and race/ethnicity

(HUNT et AL, 2008)

- Longer TL in Black Americans compared to whites (Adler et al., 2013; Hunt et al., 2008; Needham et al., 2013)
- Shorter TL in Black Americans (Diez Roux et al., 2009; Geronimus et al., 2010)
- No difference in TL among Latinxs compared to whites (Geronimus et al., 2015; Needham et al., 2013)
- Shorter TL in Latinxs (Diez Roux et al., 2009)

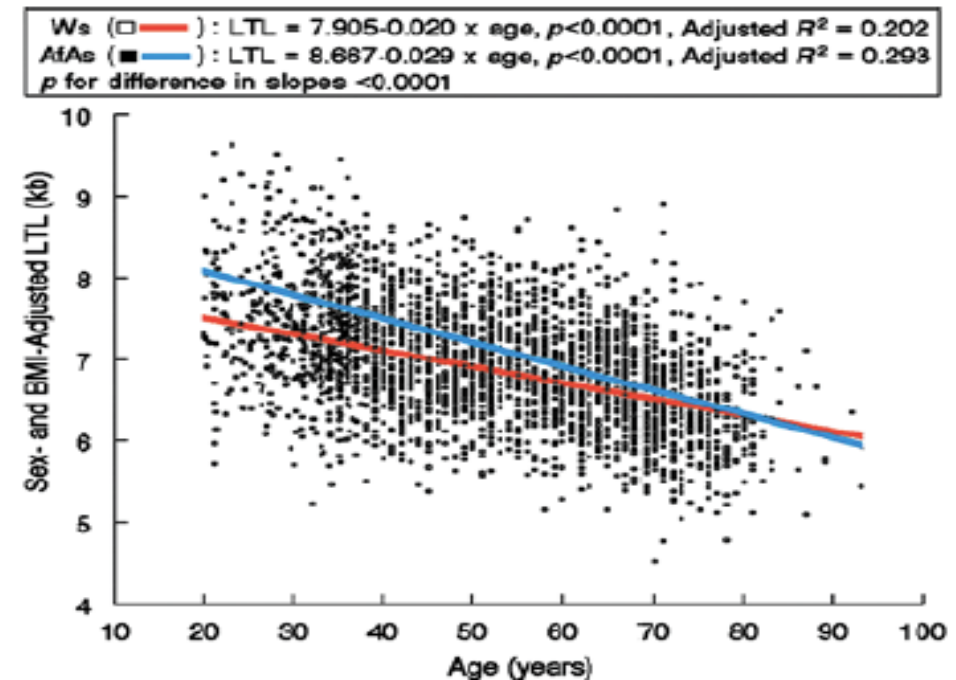


Fig. 3 Sex- and body mass index-adjusted leukocyte telomere length (LTL) vs. age for African Americans and whites from the NHLBI Family Heart Study (FHS) and the Bogalusa Heart Study (BHS) combined.

Research questions

1. Is STL a biomarker of aging that **adds to the explanatory** value of age when predicting high risk performance on indicators of biological, physical, and cognitive function in older adults?
(Brown, Zhang, Mitchell, & Ailshire, 2018)
2. Can STL be used to **identify high risk functioning** across a **diverse, nationally representative sample** or help **explain race/ethnic variability** on these same indicators of health across white, black, and Hispanic older adults? (Brown, Garcia & Ailshire, 2020)

Before adjusting for age STL predicts being high risk (n= 5,280)

- HDL Cholesterol
- Total Cholesterol
- Cystatin C
- Pulse Pressure
- BMI (obese)
- Lung function
- Walking speed

Logistic regression models adjusting for gender
and telomere assay plate

*p<0.05

**p<0.01

***p<0.001

Biomarkers	β	SE		β	SE
HDL Cholesterol	0.19	(0.10)	+		
Total Cholesterol	-0.37	(0.13)	**		
HbA1c	0.17	(0.12)			
CRP	-0.07	(0.09)			
Cystatin C	-0.36	(0.18)	*		
Systolic BP	-0.01	(0.09)			
Diastolic BP	0.06	(0.11)			
Heart Rate	-0.09	(0.18)			
Pulse Pressure	-0.23	(0.10)	*		
BMI	0.18	(0.09)	*		
Physical Performance					
Lung Function	0.36	(0.10)	***		
Walking Speed	-0.31	(0.15)	*		
Grip Strength	-0.16	(0.11)			
Balance	-0.09	(0.09)			
Cognition	-0.08	(0.12)			

Before adjusting for age
STL predicts being high risk
(n= 5,280)

- HDL Cholesterol
- Total Cholesterol
- Cystatin C
- Pulse Pressure
- BMI (obese)
- Lung function
- Walking speed

After adjusting for age
STL only predicts:

- HDL Cholesterol
- Total cholesterol
- Lung function

Logistic regression models adjusting for gender
and telomere assay plate

*p<0.05

**p<0.01

***p<0.001

Biomarkers	β	SE	+Age			SE	
			β				
HDL Cholesterol	0.19	(0.10)	+	0.19	(0.10)	*	
Total Cholesterol	-0.37	(0.13)	**	-0.45	(0.14)	**	
HbA1c	0.17	(0.12)		0.17	(0.12)		
CRP	-0.07	(0.09)		0.04	(0.09)		
Cystatin C	-0.36	(0.18)	*	-0.12	(0.16)		
Systolic BP	-0.01	(0.09)		0.08	(0.09)		
Diastolic BP	0.06	(0.11)		0.02	(0.11)		
Heart Rate	-0.09	(0.18)		-0.18	(0.19)		
Pulse Pressure	-0.23	(0.10)	*	-0.05	(0.09)		
BMI	0.18	(0.09)	*	0.09	(0.09)		
Physical Performance							
Lung Function	0.36	(0.10)	***	0.23	(0.11)	*	
Walking Speed	-0.31	(0.15)	*	0.02	(0.14)		
Grip Strength	-0.16	(0.11)		0.09	(0.11)		
Balance	-0.09	(0.09)		0.10	(0.10)		
Cognition	-0.08	(0.12)		0.10	(0.11)		

Age predicts biological,
physical, and cognitive
health before adjusting for
STL (n= 5,280)

Logistic regression models adjusting for
gender & telomere assay plate
*p<0.05 **p<0.01 ***p<0.001

Biomarkers	β	SE	β	SE
HDL Cholesterol	0.00	(0.00)		
Total Cholesterol	-0.02	(0.00)	***	
HbA1c	0.00	(0.01)		
CRP	-0.01	(0.00)	***	
Cystatin C	0.09	(0.01)	***	
Systolic BP	0.04	(0.00)	***	
Diastolic BP	-0.02	(0.00)	**	
Heart Rate	-0.04	(0.01)	***	
Pulse Pressure	0.07	(0.00)	***	
BMI	-0.05	(0.00)	***	
Physical Performance				
Lung Function	-0.09	(0.01)	***	
Walking Speed	0.15	(0.01)	***	
Grip Strength	0.10	(0.11)	***	
Balance	0.08	(0.09)	***	
Cognition	0.07	(0.12)	***	

Age predicts biological,
physical, and cognitive
health before adjusting for
STL (n= 5,280)

STL does not
explain or add to
the predictive
power of age.

Logistic regression models adjusting for
gender & telomere assay plate

*p<0.05 **p<0.01 ***p<0.001

Biomarkers	β	SE		+ TL		
				β	SE	
HDL Cholesterol	0.00	(0.00)		0.00	(0.00)	
Total Cholesterol	-0.02	(0.00)	***	-0.03	(0.00)	***
HbA1c	0.00	(0.01)		0.00	(0.01)	
CRP	-0.01	(0.00)	***	-0.01	(0.00)	***
Cystatin C	0.09	(0.01)	***	0.09	(0.01)	***
Systolic BP	0.04	(0.00)	***	0.04	(0.00)	***
Diastolic BP	-0.02	(0.00)	**	-0.02	(0.00)	**
Heart Rate	-0.04	(0.01)	***	-0.04	(0.01)	***
Pulse Pressure	0.07	(0.00)	***	0.07	(0.00)	***
BMI	-0.05	(0.00)	***	-0.05	(0.00)	***
Physical Performance						
Lung Function	-0.09	(0.01)	***	-0.09	(0.01)	***
Walking Speed	0.15	(0.01)	***	0.15	(0.01)	***
Grip Strength	0.10	(0.11)	***	0.11	(0.00)	***
Balance	0.08	(0.09)	***	0.08	(0.00)	***
Cognition	0.07	(0.12)	***	0.07	(0.01)	***

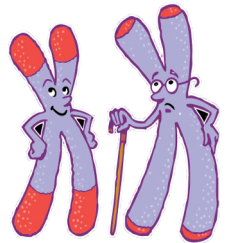
Mixed Findings: TL and indicators of health and aging

STUDIES SHOWING A RELATIONSHIP

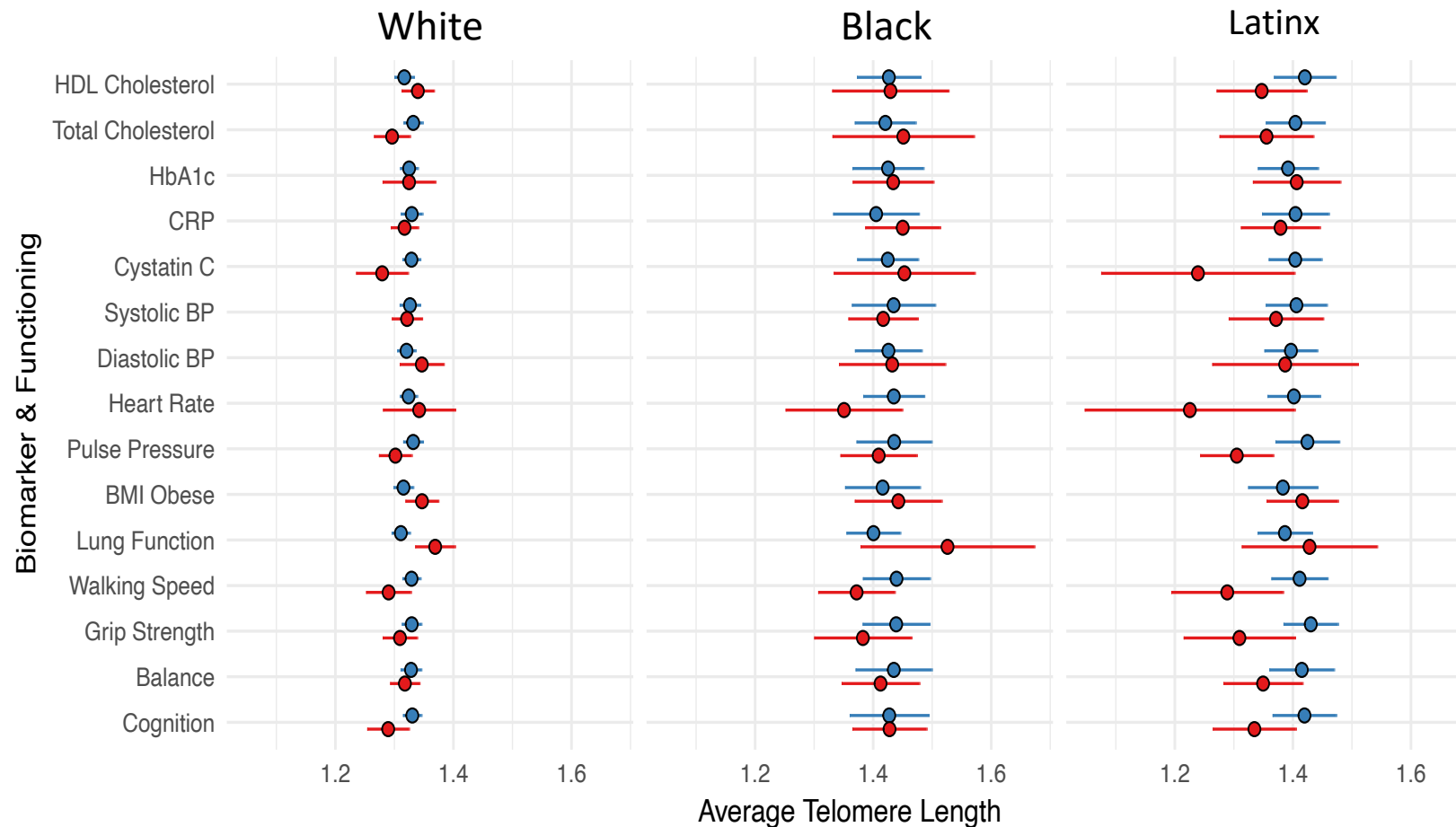
- **Inflammatory markers:** C-reactive protein (CRP), Interleukin 6 (IL-6)
(Barbieri et al., 2009; : Kaplan et al., 2009)
- **Cardiovascular markers:** pulse pressure, blood pressure (Aviv, 2001; Anstey, 1996)
- **Functioning:** lung function, handgrip strength (Bekaert et al, 2005; Karasik et al, 2005; Butler et al;. 2004)
- **Cognitive performance** (Valdes et al, 2008; Yaffe al., 2009)

STUDIES SHOWING NO RELATIONSHIP

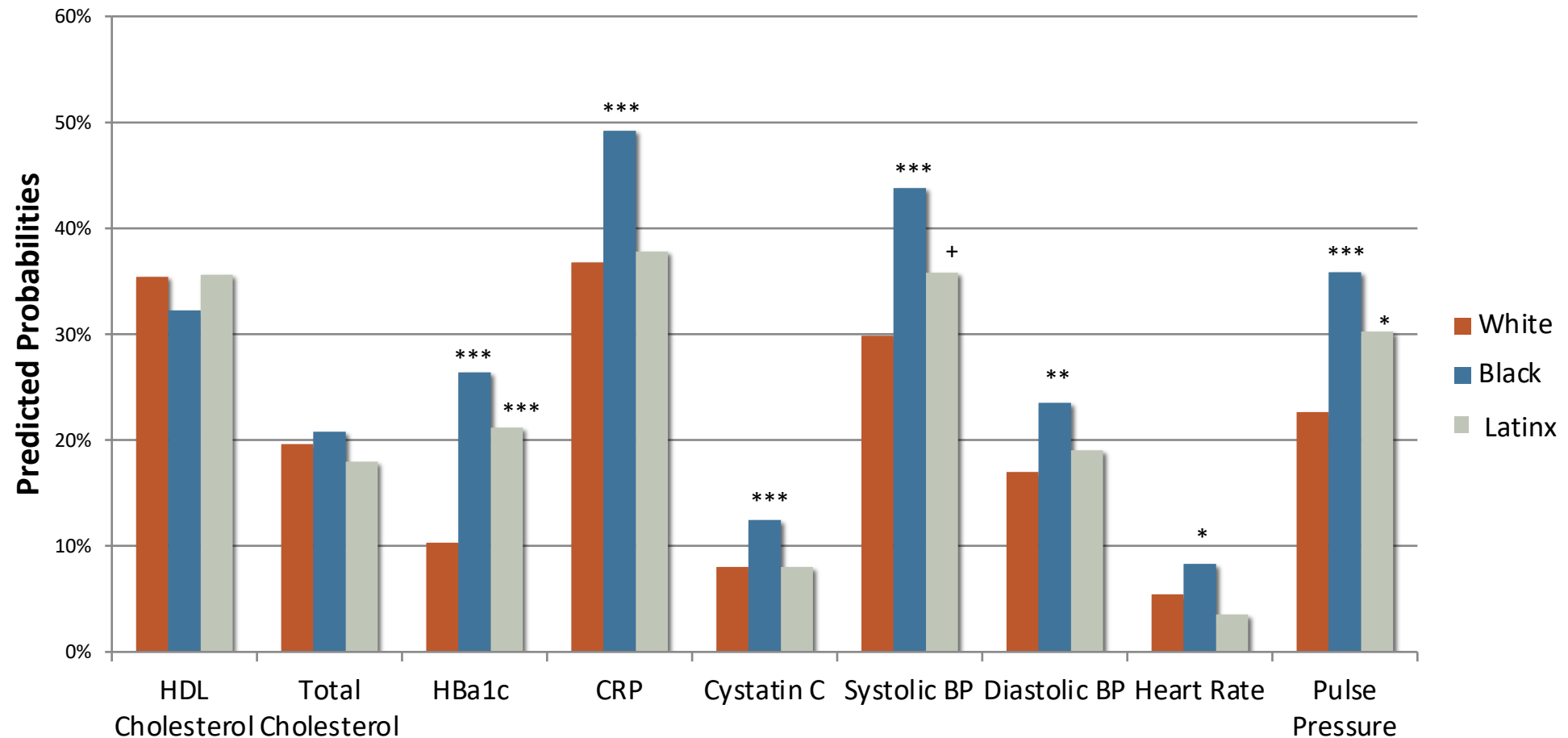
- (Sanders, 2013)
- (Mather et al, 2010)
- Fitzpatrik, 2007)
- (Mather et al, 2010)
- (Belaert et al, 2005)
- (Harris et al, 2006)
- (Harris et al, 2009)



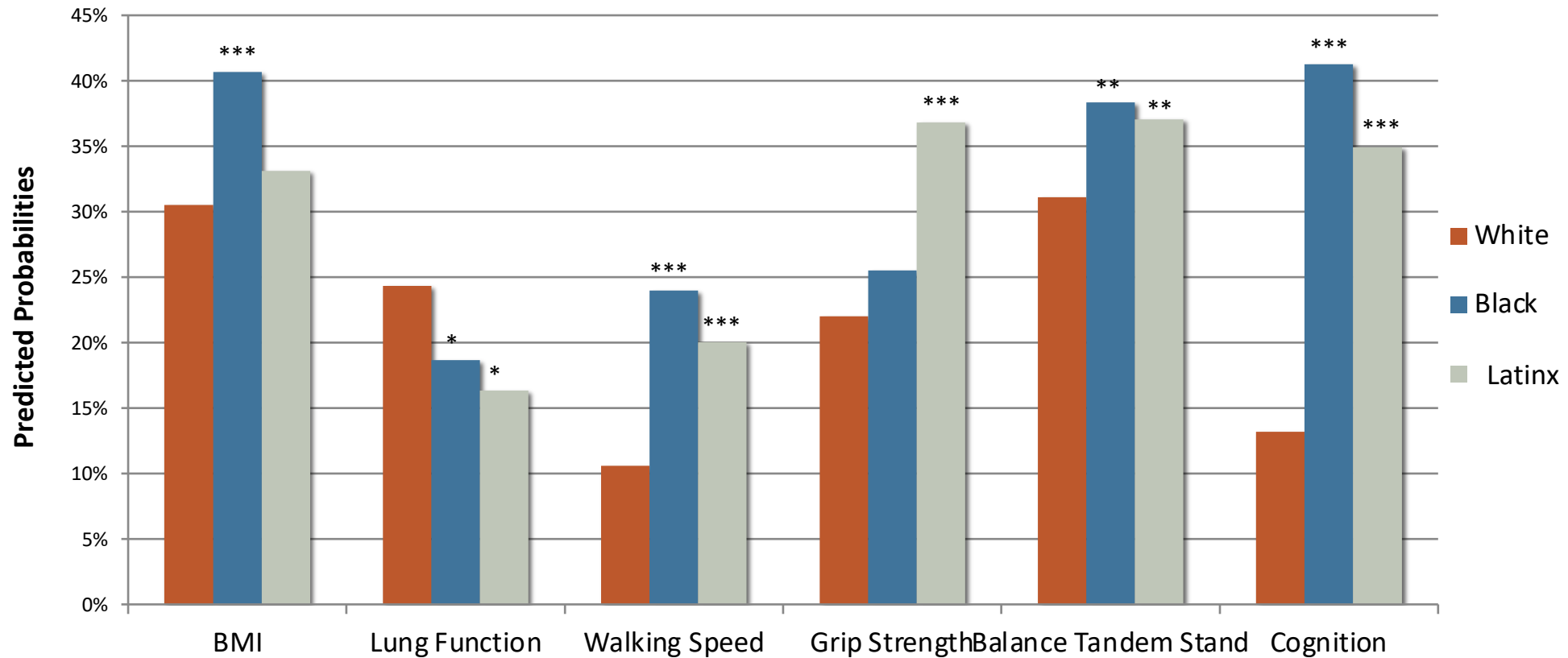
Mean STL by race/ethnicity and high vs. low risk health status (n=4,074)



TL does not explain race/ethnic differences in high risk health (n=4,074)



TL does not explain race/ethnic differences in high risk health (n=4,074)

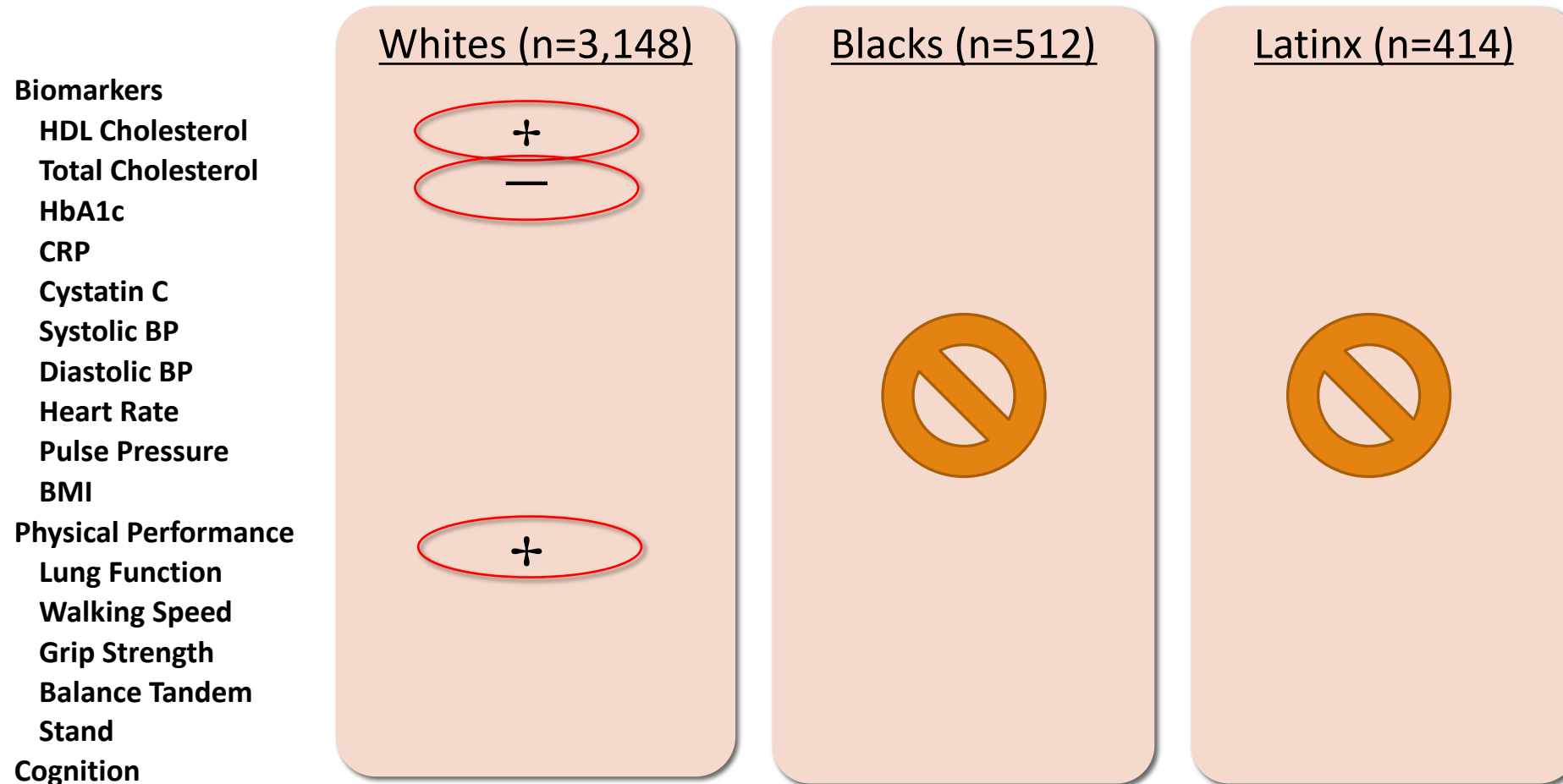


KHB method (Karlson, Holm & Breen, 2011)

Race/ethnic differences in high risk health are not attributable to the variability in STL across race/ethnic group (n=4,074)

	% Indirect	
	<u>Blacks</u>	<u>Latinx</u>
Biomarkers		
HDL Cholesterol	8.67	30.68
Total Cholesterol	33.37	17.49
HbA1c	0.58	0.38
CRP	1.34	1.58
Cystatin C	1.72	5.65
Systolic BP	0.89	0.80
Diastolic BP	2.48	1.45
Heart Rate	2.69	1.27
Pulse Pressure	0.84	0.60
BMI	2.80	2.62
Physical Performance		
Lung Function	6.71	6.71
Walking Speed	0.28	0.16
Grip Strength	1.16	0.13
Balance Tandem	2.12	0.69
Cognition	0.32	0.15

Stratified models: STL predicts indicators of health only among whites



TL did not predict nor account for race/ethnic variation in health and functioning

- Race/ethnic stratified models suggest that TL may better characterize health and functioning among older whites
- Race/ethnic variation in STL did not explain race/ethnic variation in health and functioning
- STL in the HRS— measured cross-sectionally in saliva and quantified by qPCR— is not a biomarker of aging that helps us understand race/ethnic differences in older adulthood.
- It maybe worth questioning the value of including STL in large nationally representative studies of older adults.



How do we explain mixed findings in TL?

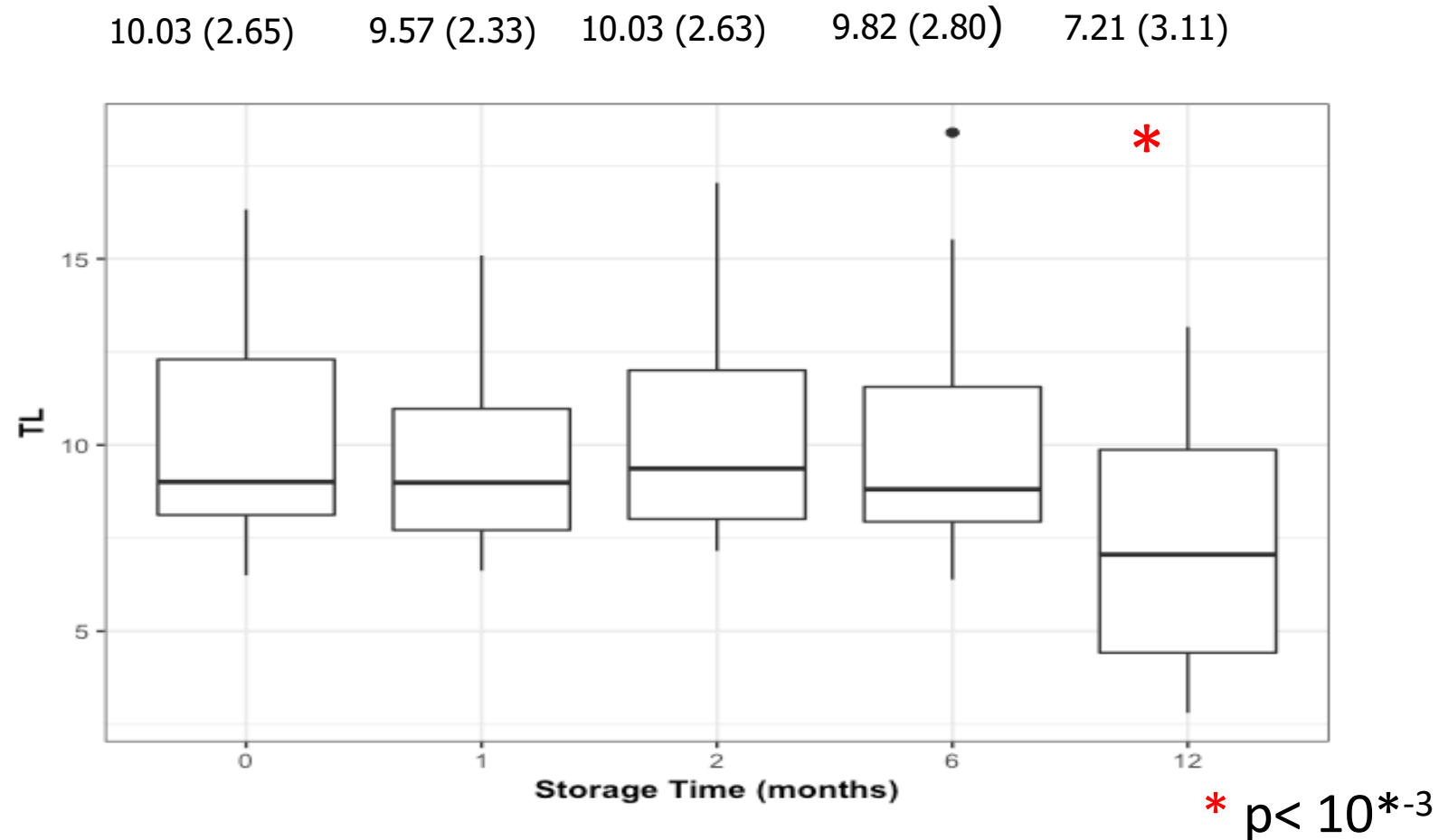
Methodical issues

- Cross-sectional data
 - Change more important than absolute TL ?
- Cell type (salvia vs blood)
- Assay (qPCR, southern blot)
- Sample size
- Homogenous samples (race/ethnicity, age, geography)

Highly heritable trait (estimates range from 0.36 to 0.82) (Andrew et al. 2006; Honig et al. 2015)

- Black Americans are born with longer TL (Drury et al., 2015; Rewak et al., 2014)

HRS: Measured STL by storage month (at room temp before extraction) (Faul et al, unpublished)



HRS 2008 TL data & social factors:

Studies have found links with

- Social relationships (Lincoln, Lloyd & Nguyen, 2017)
- Religious involvement (Hill et al, 2017)
- Discrimination (Liu & Kawachi, 2017; Lee, Kim & Neblett, 2017)
- Depressive symptoms (Whisman & Richardson, 2017)
- Lifespan adversity (Puterman et al, 2016; Willis et al, 2019)
- Marital disruption (Whisman et al, 2016)

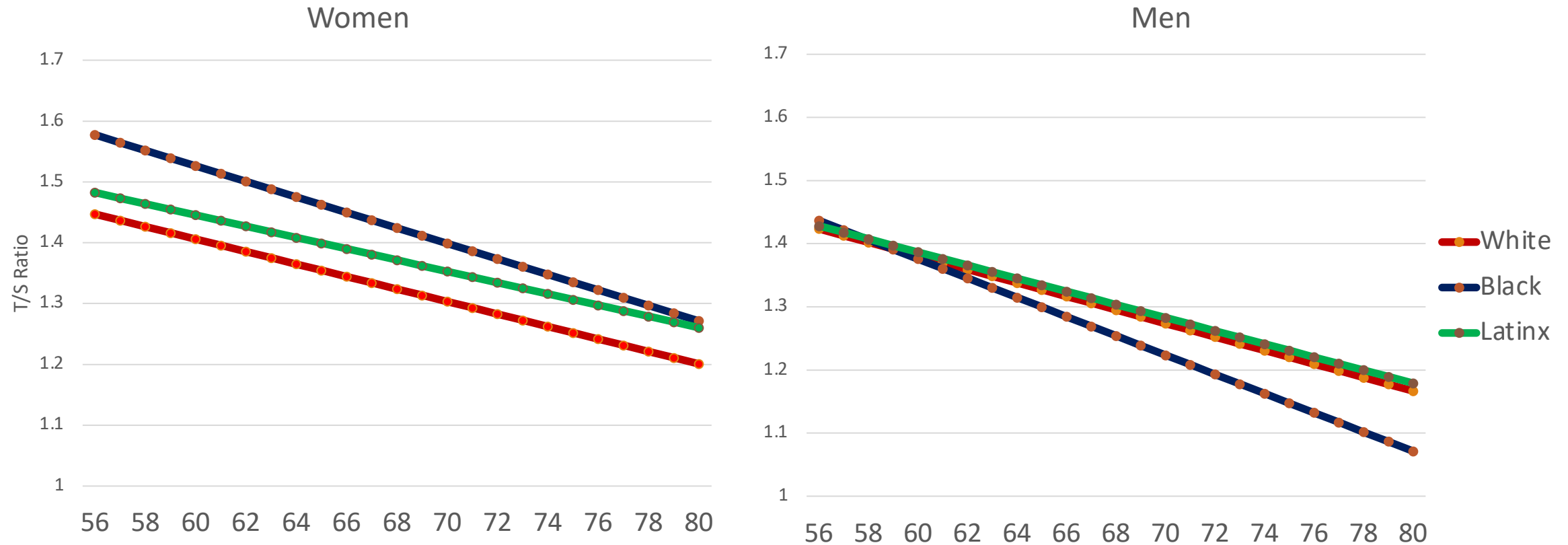


2016 HRS Venous Blood Study

- Re-assayed TL from new subsample using venous blood
 - 10mL EDTA (whole blood)
 - Storage: 3.5 mL plasma Buffy coat Extracted DNA
- Real time PCR
- T/S Ratio
 - the ratio of copies of telomere specific sequence to a nuclear gene (albumin) copy number will be determined for each sample and standardized to a reference DNA sample to adjust for assay variability.
- CV= 8%.



2016 VBS: Older Black women have longer TL (n=3,853)



Inequalities in health exacerbated by molecular based biomarkers?

- **79 % of all GWAS participants are European Ancestry** (Martin et al, 2018)
 - despite making up 16% of global population
- **Polygenic risk scores perform better in European populations** (Martin et al, 2018)
- **African and Asian ancestry**
 - more likely to receive ambiguous genetic test results
 - More likely to have variants of unknown significance (Petrovski & Goldstein, 2016)
- **African ancestry**
 - more likely to be wrongly told that a mutation increases their risk of developing disease (Manrai et al, 2016)

Certain drugs may be less effective, or even unsafe, in some populations because of genetic differences.

Genomics is failing on diversity

An analysis by Alice B. Popejoy and Stephanie M. Fullerton indicates that some populations are still being left behind on the road to precision medicine.

A 2009 analysis revealed that 96% of participants in genome-wide association studies (GWAS) were of European descent¹. Such studies scan the genomes of thousands of people to find variants associated with disease traits. The find-

analysis. Our findings indicate that the proportion of individuals included in GWAS who are not of European descent has increased to nearly 20%. Much of this rise, however, is a result of more studies being done in Asian populations of Asian

US National Institutes of Health (NIH) mandated the inclusion of diverse participants in the biomedical research it funds, GWAS funded by the NIH and other sources are continuing to miss a vast portion of the world's genetic variation

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